

REMARKS

Claims 1-48 and 50-59 are pending in the present application. Reconsideration is respectfully requested in view of the following comments and the amendments above.

The rejection of Claims 45-46 and 49 under: (a) 35 U.S.C. §112, first paragraph (written description), and (b) 35 U.S.C. §112, second paragraph, are obviated by amendment.

The primary basis for this ground of rejection is the Examiner's indication that SEQ ID NO: 80 is not an amino acid sequence and that SEQ ID NO: 79 is not a full-length open reading frame. Applicants wish to thank Examiner Navarro for bringing this error to their attention. Applicants note that the Sequence Listing as originally presented contains the appropriate sequences bearing the identifiers SEQ ID NO: 79 and SEQ ID NO: 80. However, upon submission of the substitute Sequence Listing on December 27, 2002, the first nucleotide ("g") in SEQ ID NO: 23 was inadvertently omitted. This error gave rise to a frame-shift resulting in the introduction of several internal stop codons and an increase in the number of open reading frames. As a result, SEQ ID NO: 79 appearing in the substitute Sequence Listing on December 27, 2002, actually corresponds to original SEQ ID NO: 58 and SEQ ID NO: 80 appearing in the substitute Sequence Listing on December 27, 2002, actually corresponds to original SEQ ID NO: 59.

To correct the error above, and to obviate the primary basis for these grounds of rejection, Applicants **submit herewith** a corrected substitute Sequence Listing and a corresponding computer-readable Sequence Listing. The sequence information recorded in the corresponding computer-readable Sequence Listing is identical to the paper copy of the corrected substitute Sequence Listing. Support for all of the sequences listed in the corrected substitute Sequence Listing is found in the present application. No new matter is believed to

have been introduced by the submission of the corrected substitute Sequence Listing and the corresponding computer-readable Sequence Listing.

Further, also to address a criticism by the Examiner, Applicants have amended the claims to limit the number of substitutions, deletions, insertions, additions, or inversions in the amino acid sequence to 1 to 10 (see new Claim 50). In addition, the stringent conditions have been defined as being "60°C, 1 x SSC and 0.1% SDS" and the claimed DNA has been limited to encoding a protein having a homology of 90% or more compared to SEQ ID NO: 80.

In view of the foregoing, withdrawal of these grounds of objection is requested.

The rejection of Claims 45, 46, and 49 under 35 U.S.C. §102(b) over Eikmanns et al is obviated by amendment.

Applicants note that with the correction of the Sequence Listing, Eikmanns et al fail to disclose or suggest the sequences corresponding to SEQ ID NOs: 79 and 80. Further, Eikmanns et al fail to disclose or suggest any sequences falling within the range of permissible mutation and/or homology, as well as the specific stringent conditions.

Accordingly, in view of the present amendment, Applicants submit that Eikmanns et al fail to anticipate the claimed invention and this ground of rejection should be withdrawn. Acknowledgment to this effect is requested.

The rejection of Claim 46 under 35 U.S.C. §112, second paragraph, is obviated by amendment.

Applicants have amended the claims to be free of the Examiner's criticisms. More specifically, the claims have been amended to define the "stringent conditions" as "60°C, 1 x SSC and 0.1% SDS."

In view of the amendments herein, withdrawal of this rejection is respectfully requested.

The rejection of Claims 45-46 under 35 U.S.C. §101 is obviated by amendment. Applicants have amended the claims to recite "an isolated DNA" so as to specifically indicate the involvement of the "hand of man." Accordingly, this ground of rejection is no longer believed to be tenable.

Withdrawal of this ground of rejection is requested.

Applicants submit that the application is in condition for allowance. Early notice to this effect is earnestly solicited.

Respectfully submitted,

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